

Figure 1A.

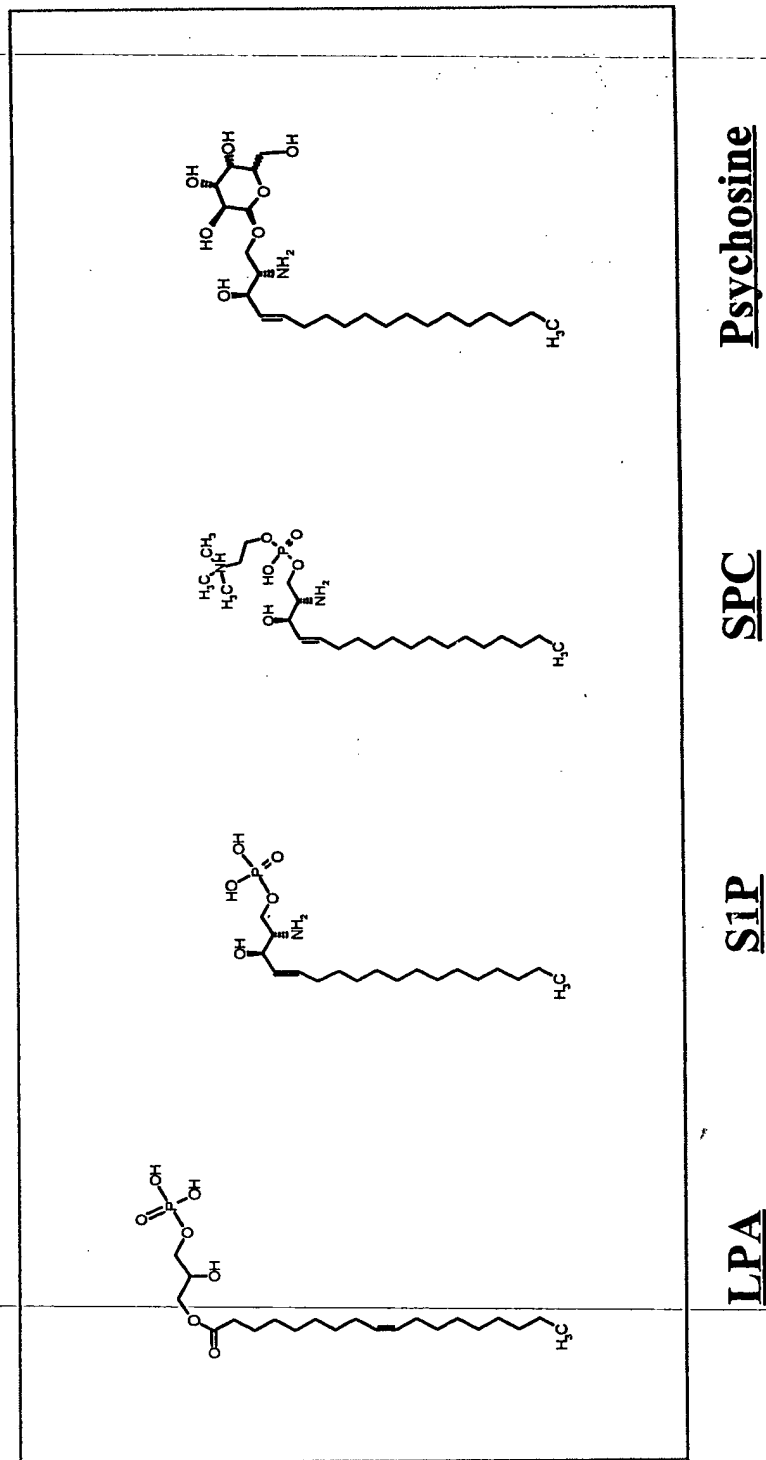


Figure 1B.

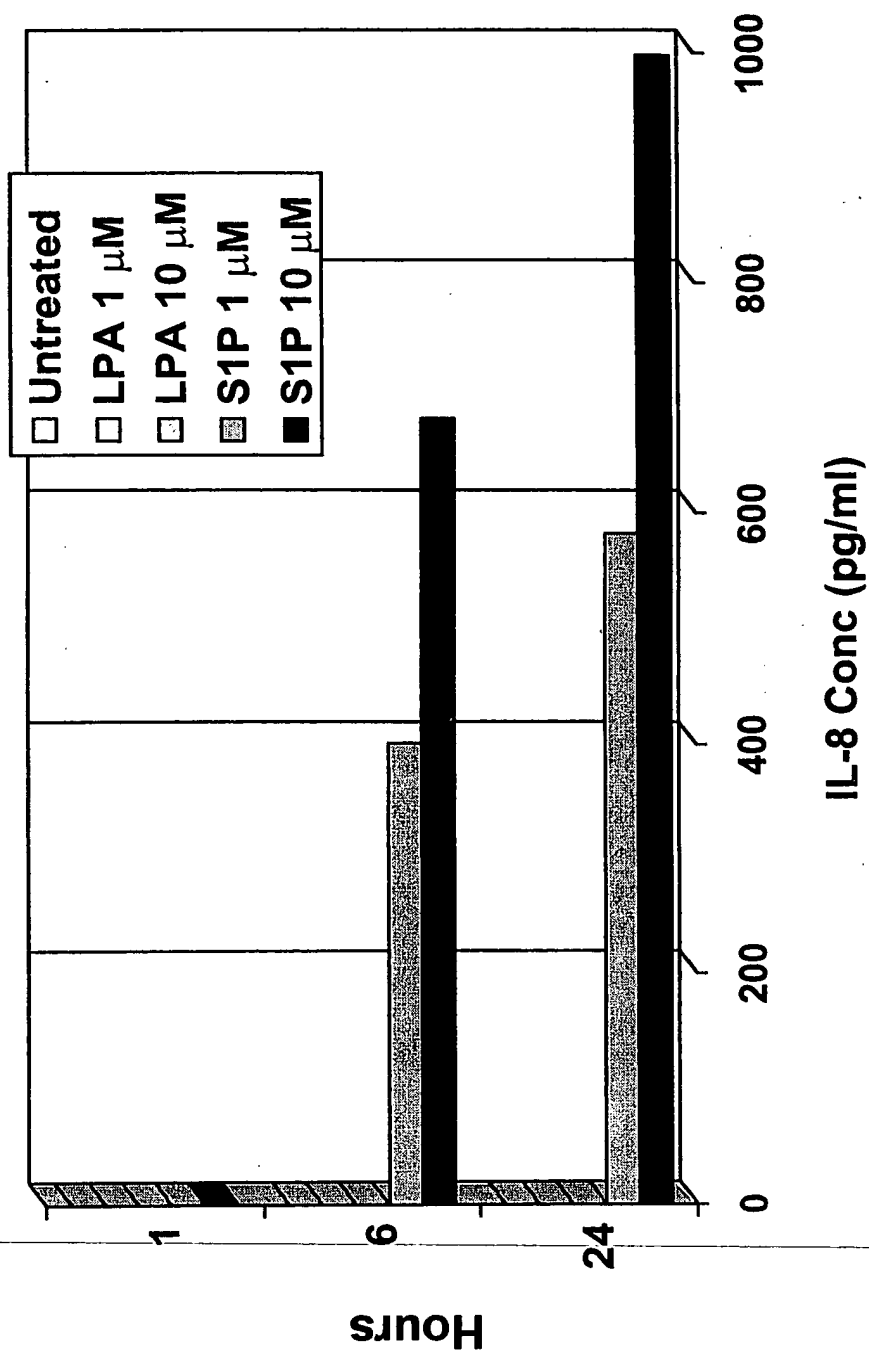
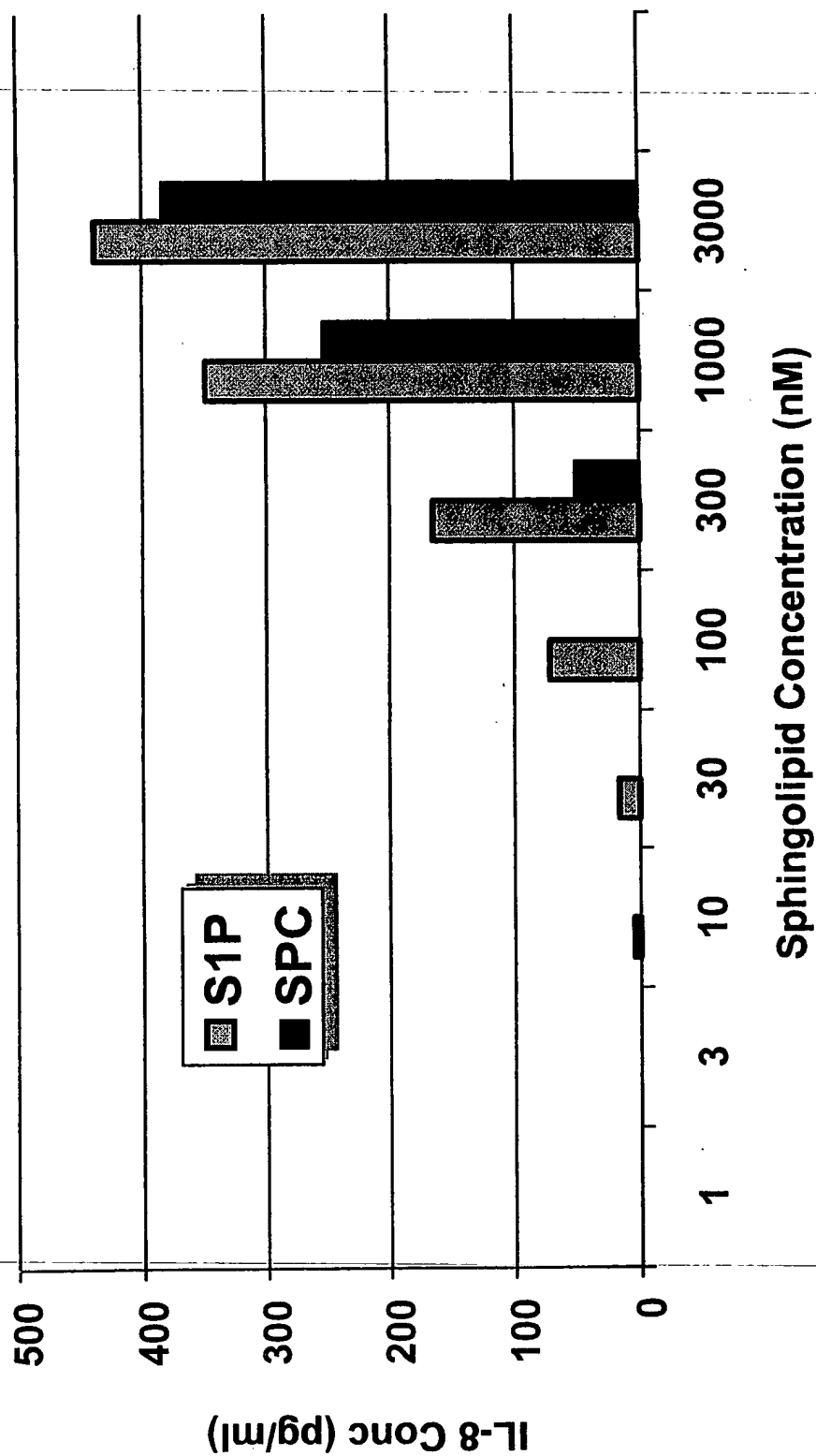


Figure 2A.



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FIGURE 2

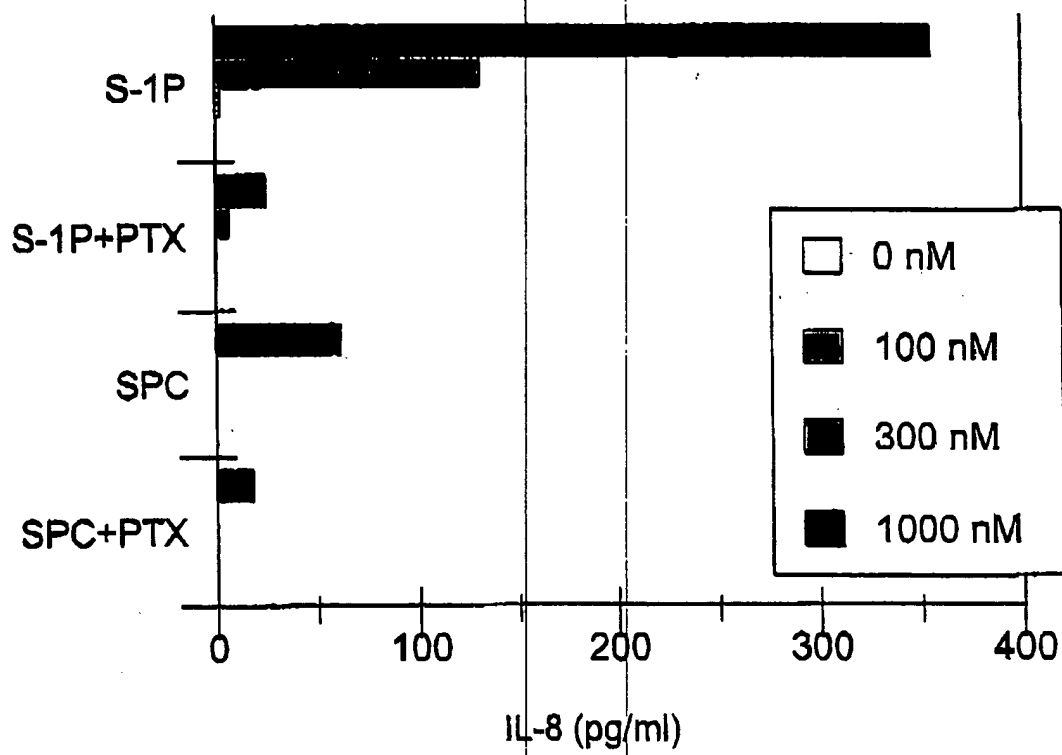
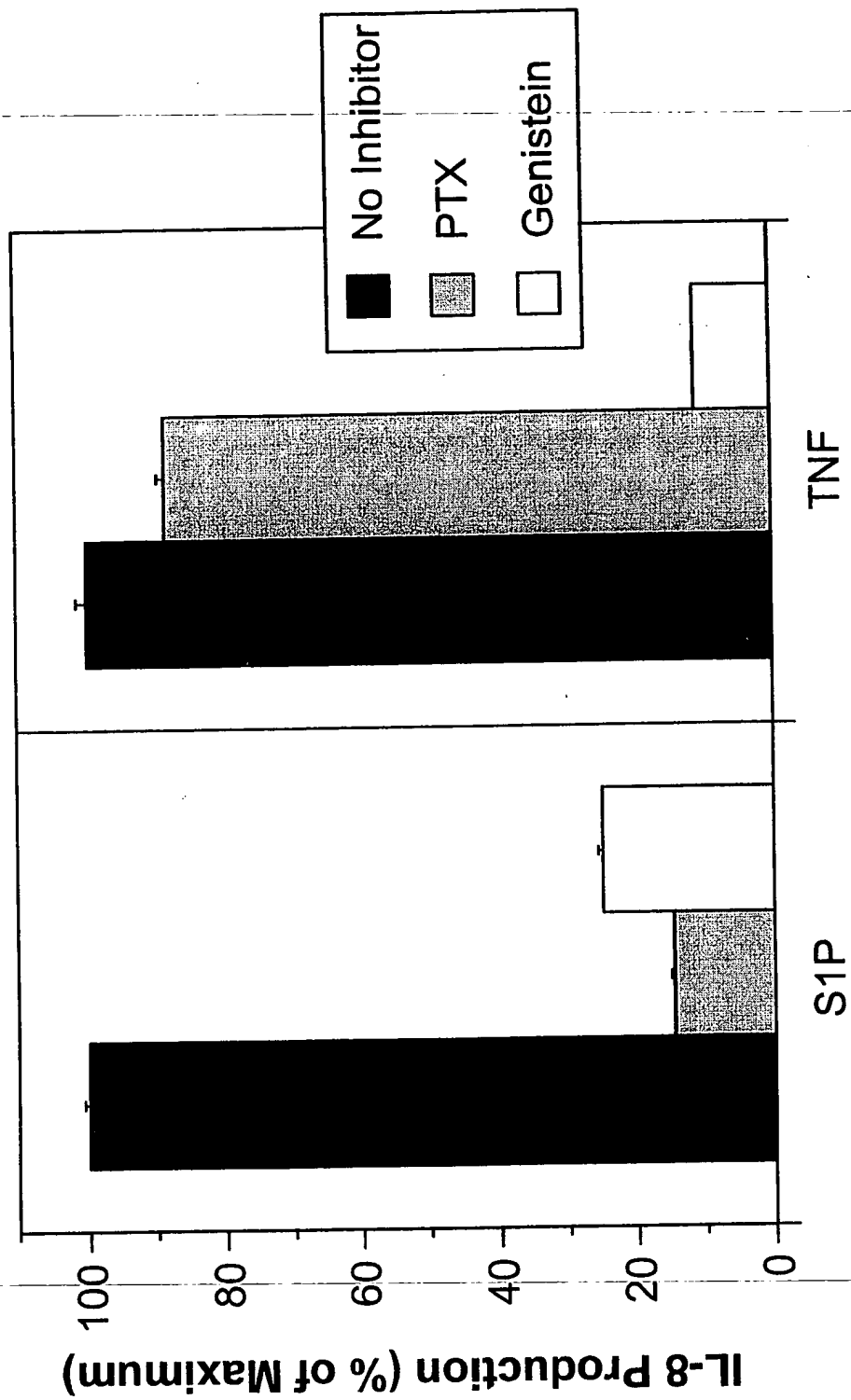


Figure 3.



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FIGURE 4A

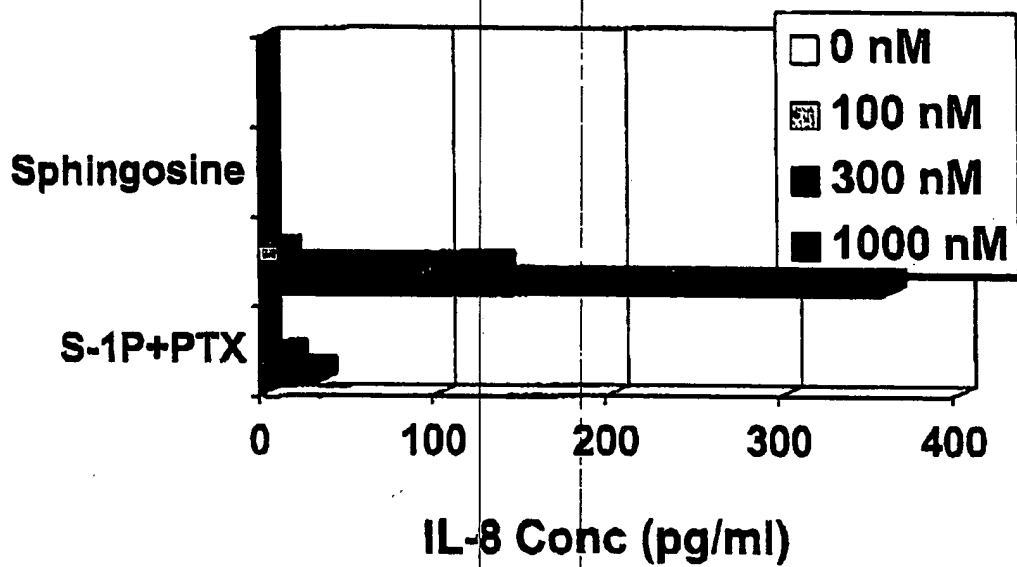


Figure 4B.

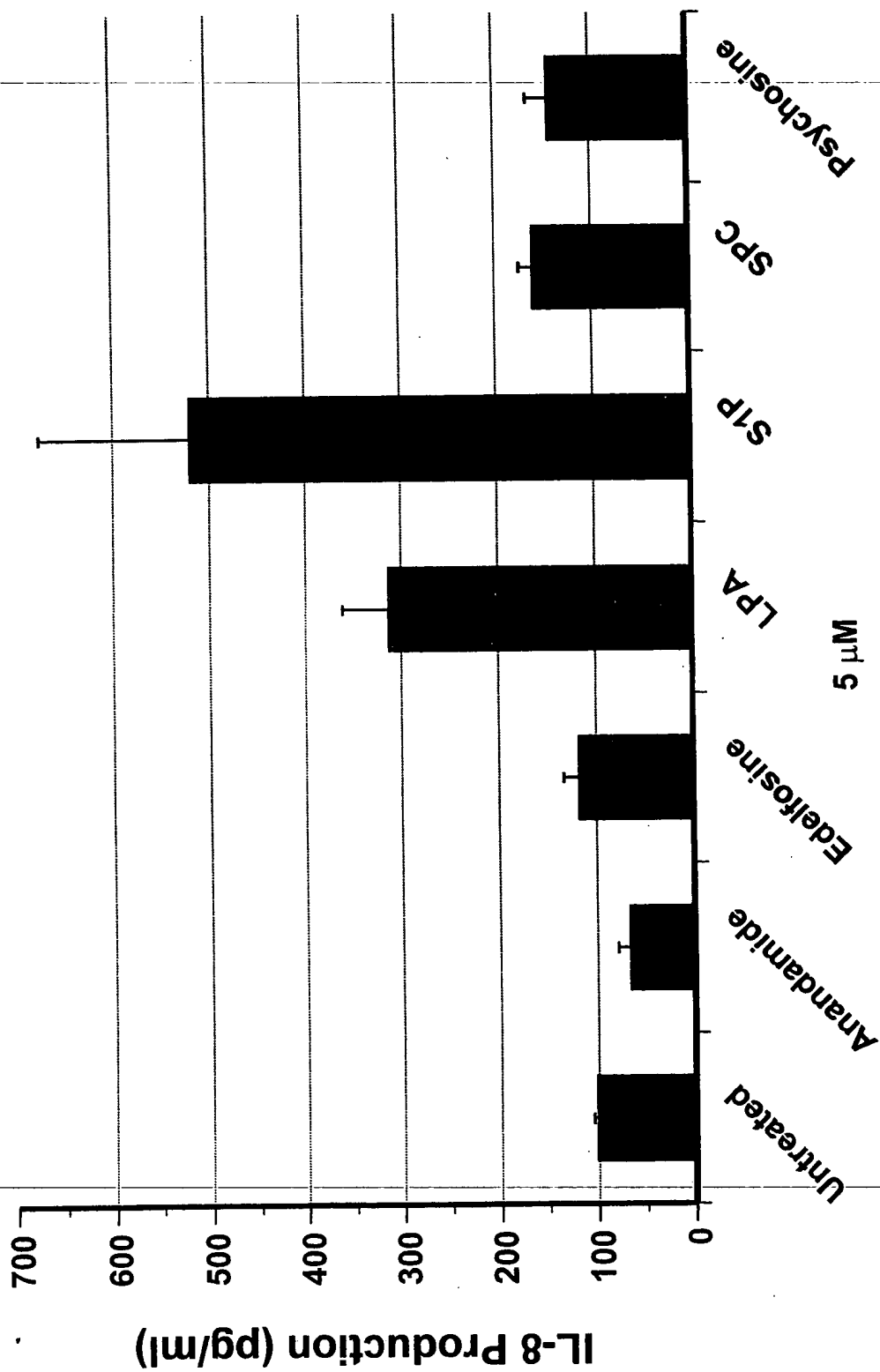
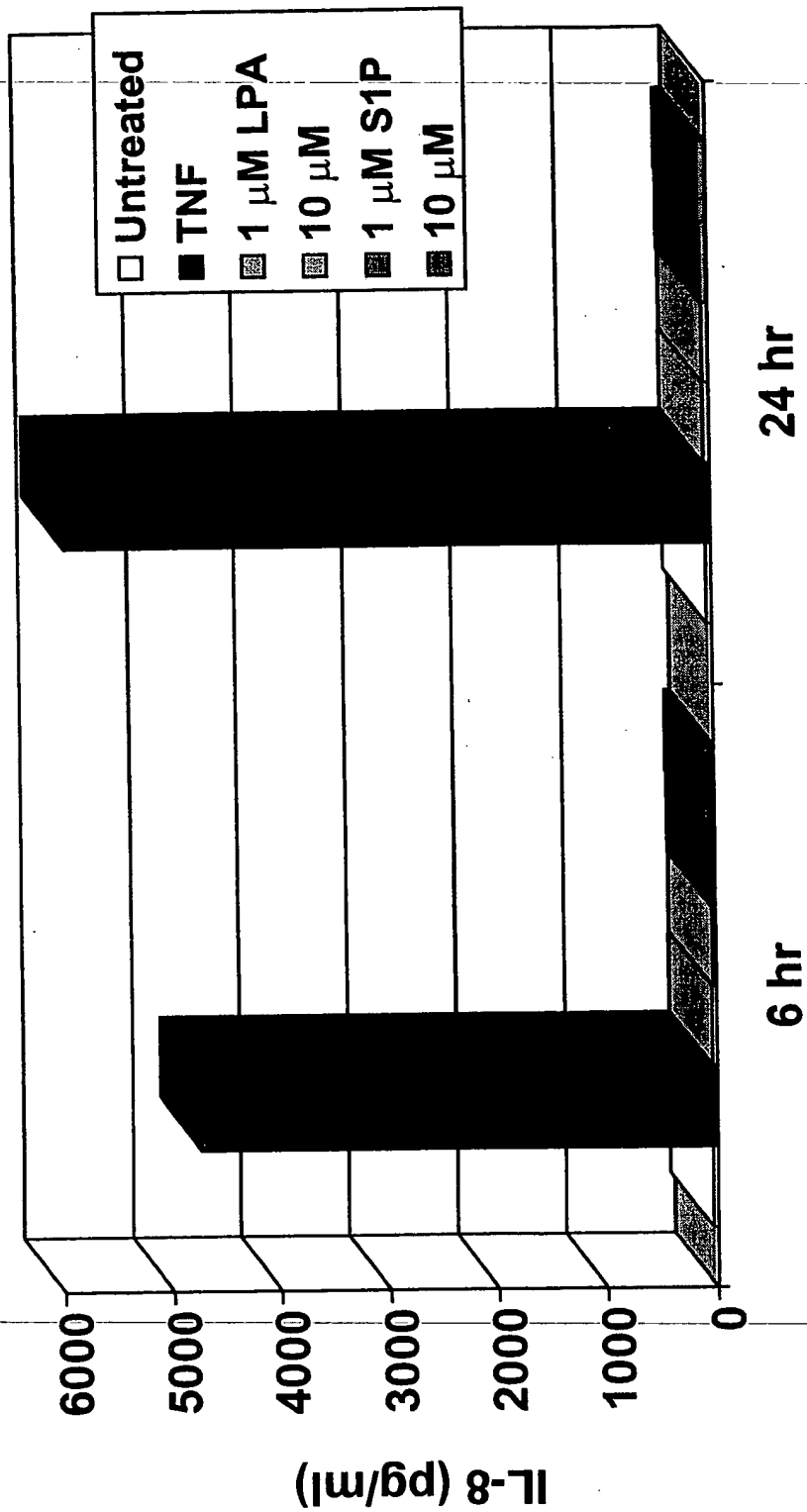


Figure 5.



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Figure 6.

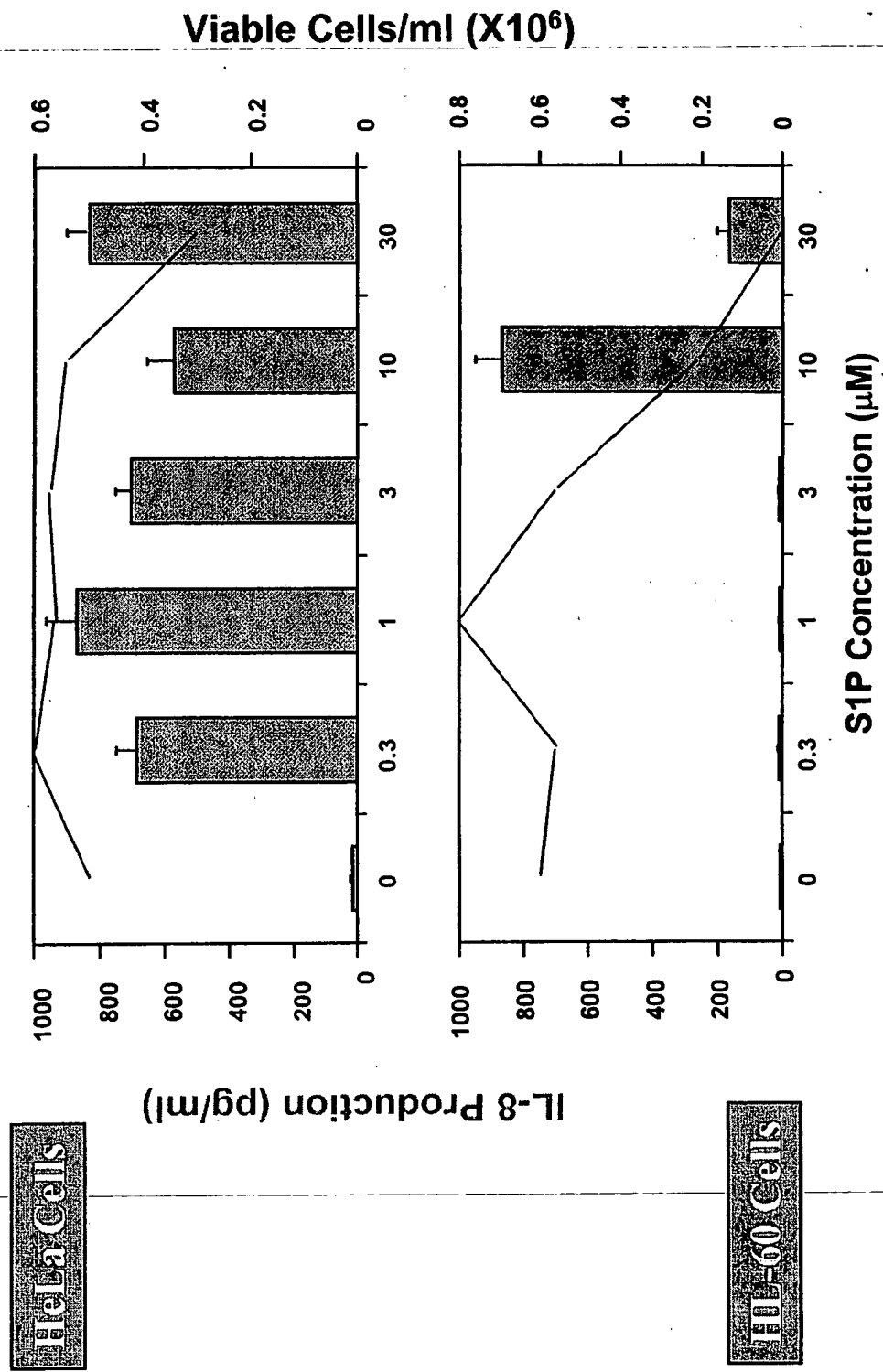


Figure 7.

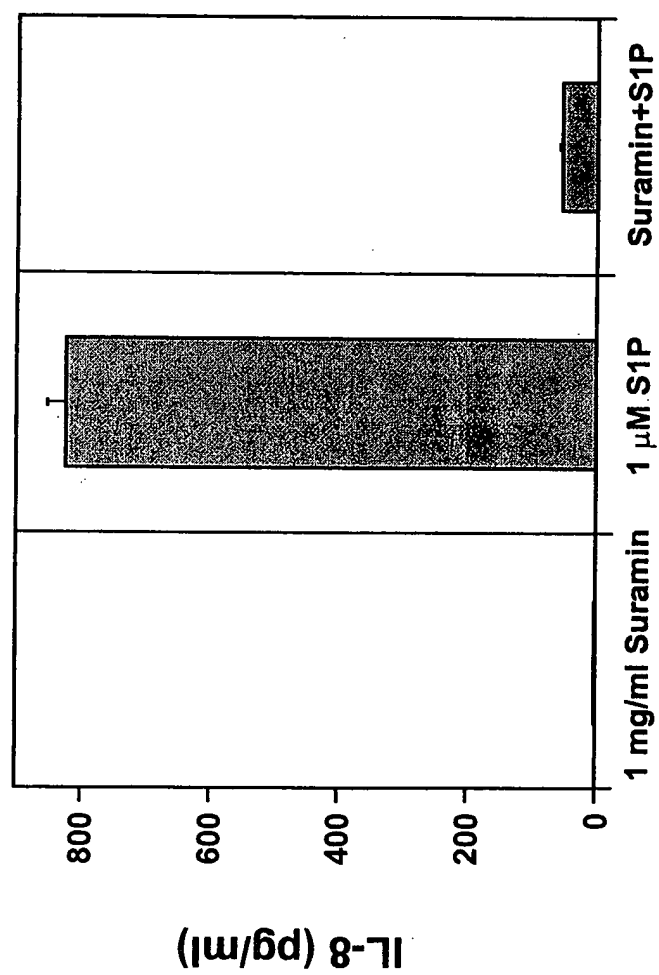


Figure 8.

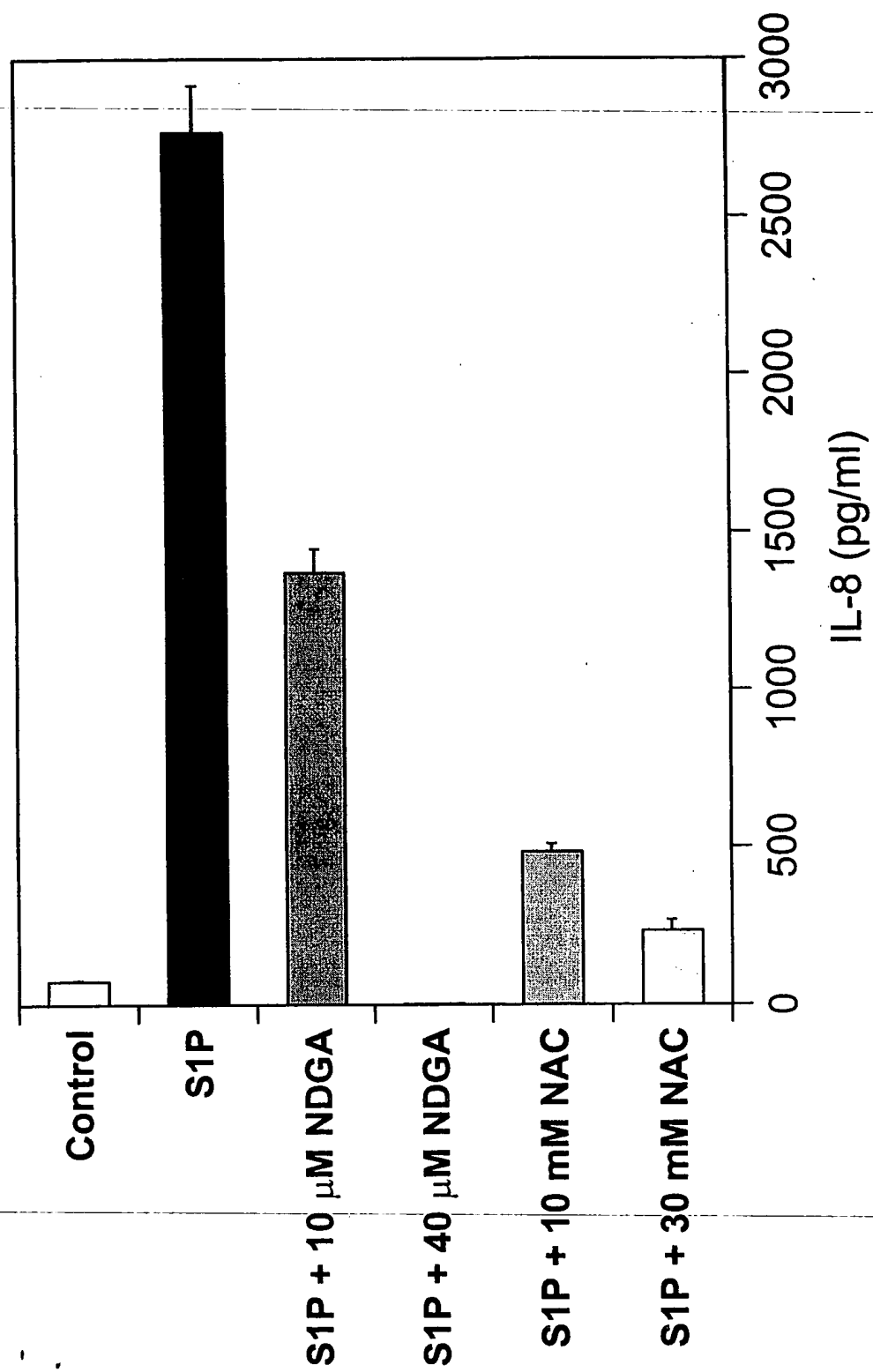
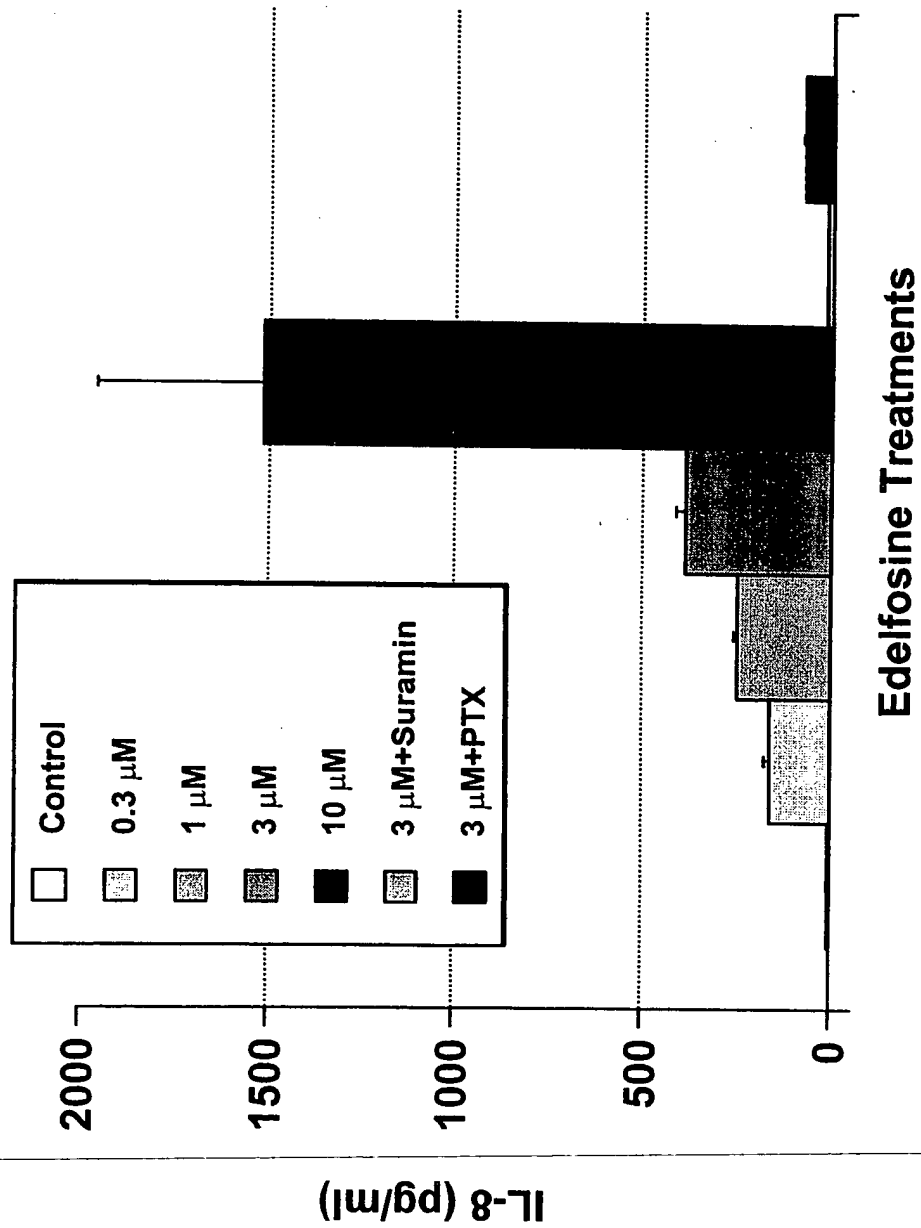


Figure 9.



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FIGURE 10A

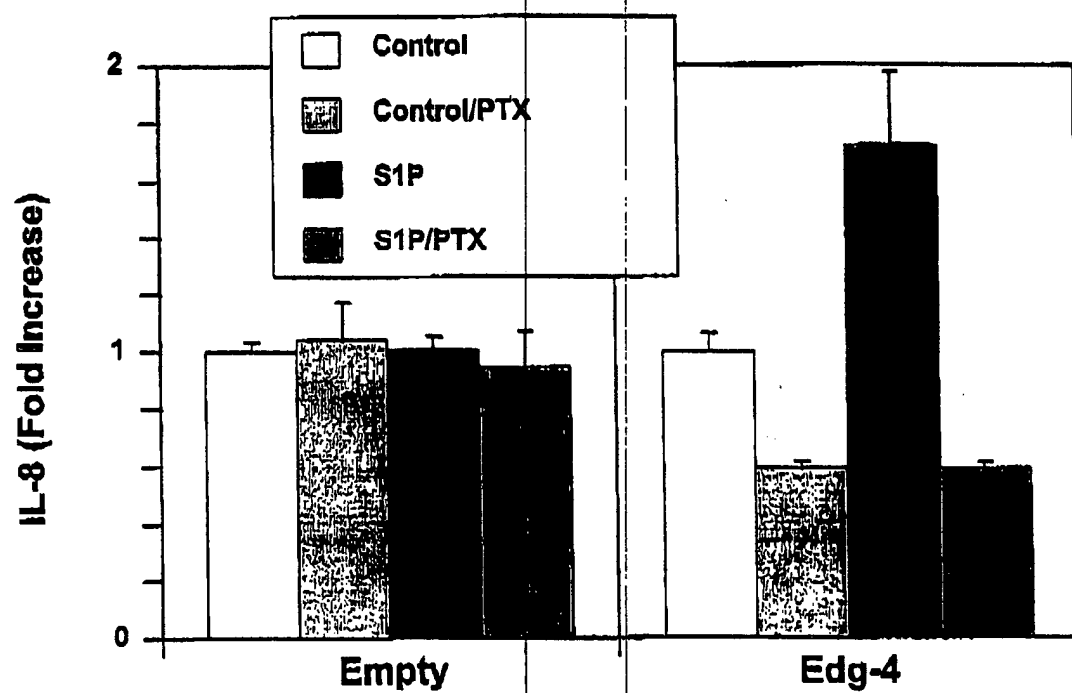


Figure 10B

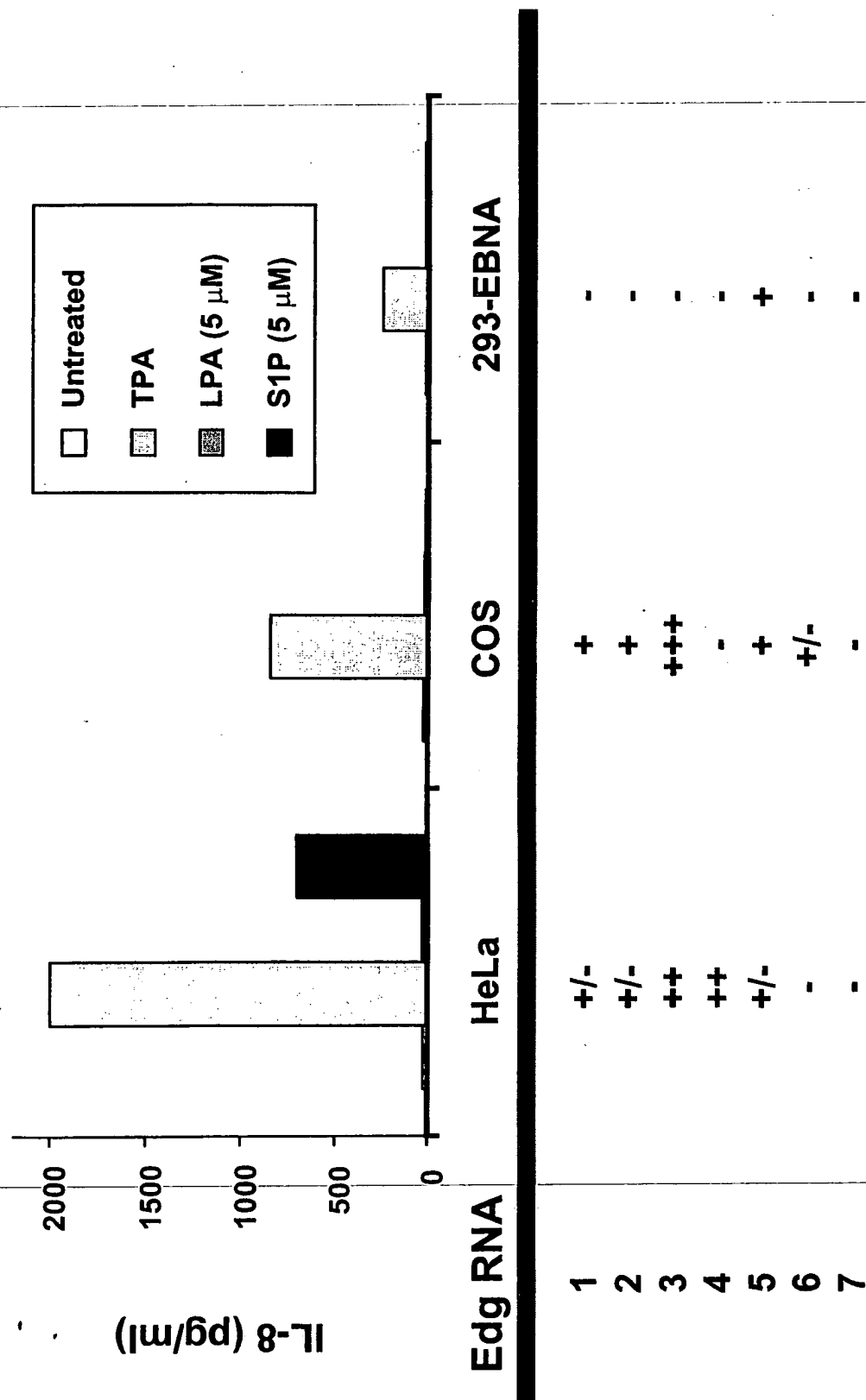


Figure 11.

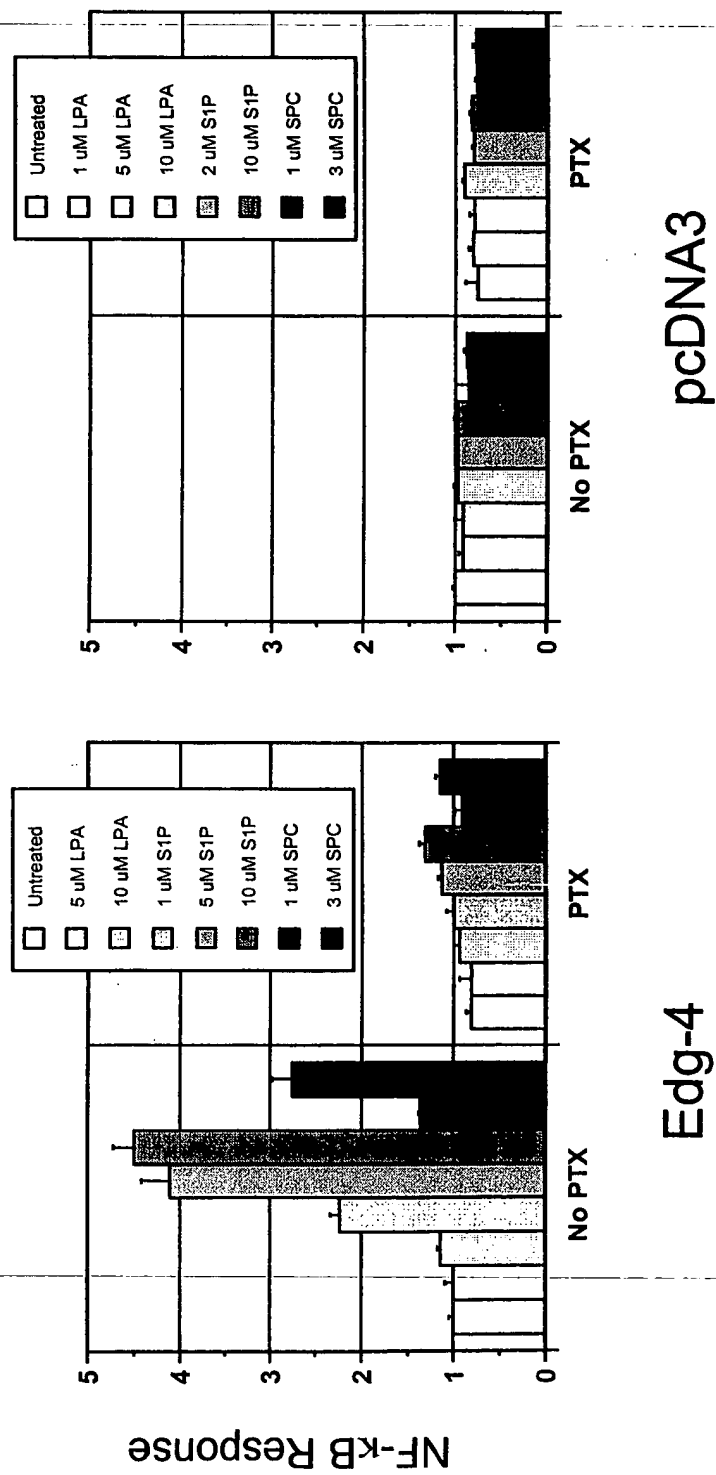


Figure 12.

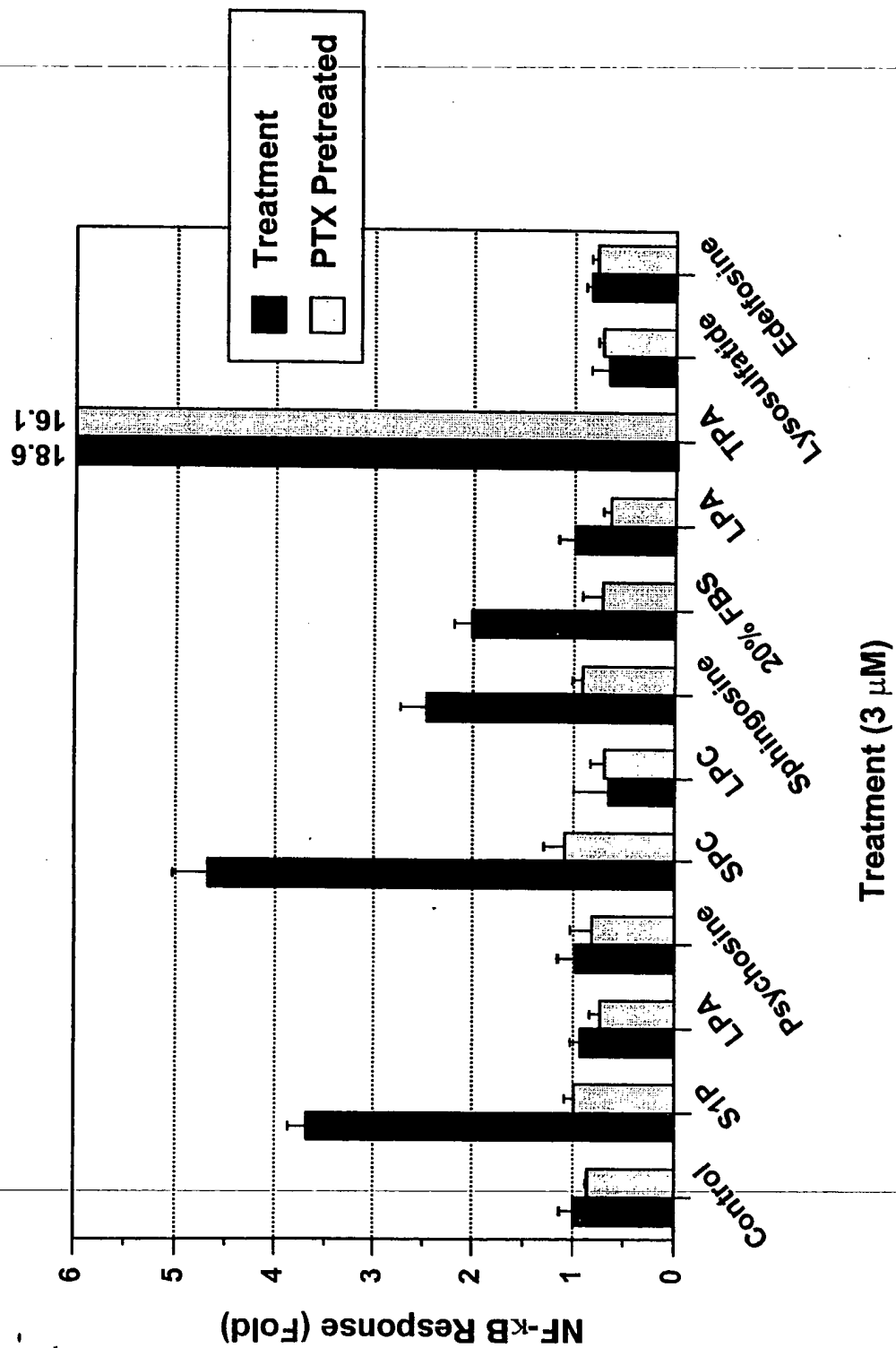


Figure 13.

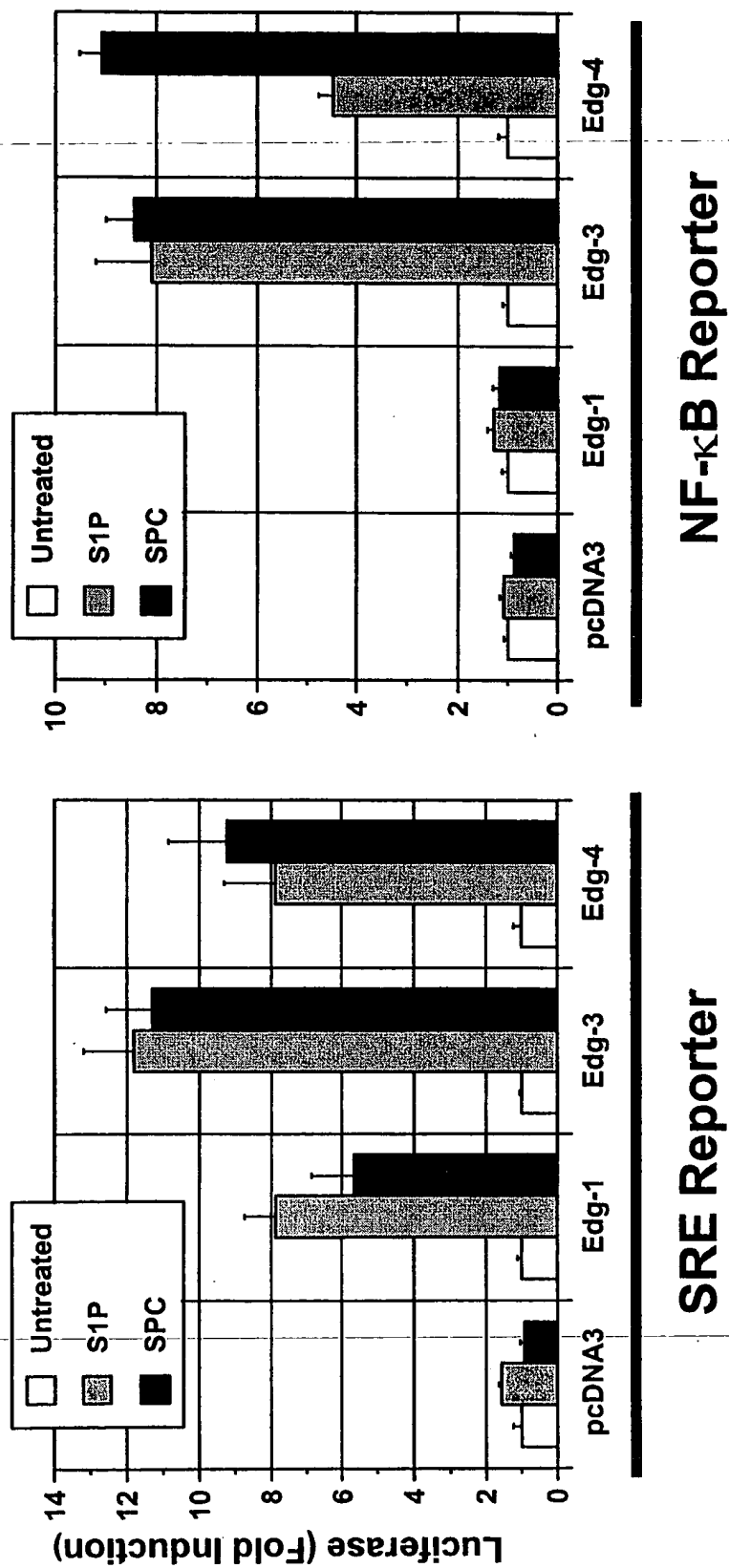


FIGURE 14

1				50
AA834537	-----AAA	GCCCCATGGC	CCCAGCAGGC	CTCTGAGCCC CACCATGGGC
AA804628	-----AAA	GCCCCATGGC	CCCAGCAGGC	CTCTGAGCCC CACCATGGGC
AA827835	AGTTCTGAAA	GCCCCATGGC	CCCAGCAGGC	CTCTGAGCCC CACCATGGGC
	51			100
AA834537	AGCTTGTACT	CGGAGTACCT	GAACCCCAAC	AAGGTCCAGG AACACTATAA
AA804628	AGCTTGTACT	CGGAGTACCT	GAACCCCAAC	AAGGTCCAGG AACACTATAA
AA827835	AGCTTGTACT	CGGAGTACCT	GAACCCCAAC	AAGGTCCAGG AACACTATAA
	101			150
AA834537	TTATACCAAG	GAGACGCTGG	AAACGCAGGA	GACGACCTCC CGCCAGGTGG
AA804628	TTATACCAAG	GAGACGCTGG	AAACGCAGGA	GACGACCTCC CGCCAGGTGG
AA827835	TTATACCAAG	GAGACGCTGG	AAACGCAGGA	GACGACCTCC CGCCAGGTGG
	151			200
AA834537	CCTCGGCATT	CATCGTCATC	CTCTGTTGCG	CCATTGTGGT GGAAAACCTT
AA804628	CCTCGGCCTT	CATCGTCATC	CTCTGTTGCG	CCATTGTGGT GGAAAACCTT
AA827835	GCTCGGCCTT	CATCGTCATC	CTCTGTTGCG	CCATTGTGGT GGAAAACCTT
	201			250
AA834537	CTGGTGCTCA	TTGCGGTGGC	CCGAAACAGC	AAGTTCCACT CGGCAATGTA
AA804628	CTGGTGCTCA	TTGCGGTGGC	CCGAAACAGC	AAGTTCCACT CGGCAATGTA
AA827835	CTGGTGCTCA	TTGCGGTGGC	CCGAAACAGC	AAGTTCCACT CGGCAATGTA
	251			300
AA834537	CCTGTTTCTG	GGCAACCTGG	CGGCCTCCGA	TCTACTGGCA GGCCTGGCCT
AA804628	CCTGTTTCTG	GGCAACCTGG	CGGCCTCCGA	TCTACTGGCA GGCCTGGCCT
AA827835	CCTGTTTCTG	GGCAACCTGG	CGGCCTCCGA	TCTACTGGCA GGCCTGG .CT
	301			350
AA834537	TCGTAGCCAA	TACCTTGCTC	TCTGGCTCTG	TCACGCTGAG GCTGACGCCT
AA804628	TCGTAGCCAA	TACCTTGCTC	TCTGGCTCTG	TCACGCTGAG GCTGACGCCT
AA827835	TCGTAGCCAA	TACCTTGCTC	TCTGGCTCTG	TCACGCTGAG GCTGACGCCT
	351			400
AA834537	GTGCAGTGGT	TTGCCCGGGA	CGGTCTGCCT	TCATCAGGCT CTCGGCCTCT
AA804628	GTGCAGTGGT	TTGCCCGGGA	C-----	-----
AA827835	GTGCAGTGGT	TTGCCCGGGA	-----	-----
	401			450
AA834537	GTCTTCAGCC	TCCTGGCCAT	CGCCATTGAG	CGCCACGTGG CCATTGCAAA
AA804628	-----	-----	-----	-----
AA827835	-----	-----	-----	-----
	451			
AA834537	GG			
AA804628	--			
AA827835	--			

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FIGURE 15 A

N G S L Y S E Y

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1  AAAGCCCCATGGCCCCAGCAGGCTCTGAGCCCCACCATGGGCAGCTTGTACTCGGAGTA
   -----+-----+-----+-----+-----+-----+-----+-----+
61  TTTCGGGGTACCGGGTTCGTCCGAGACTCGGGGTGGTACCCGTGGAACATGAGCCTCAT
   -----+-----+-----+-----+-----+-----+-----+-----+
   L N P N K V Q E E Y N Y T K E T L E T Q
   CCTGAACCCCAACAGGTCCAGGAACACTATAATTATACCAAGGAGACGCTGGAAACGCA
   -----+-----+-----+-----+-----+-----+-----+-----+
121  GGACTTGGGGTTGTTCCAGGTCCTTGTGATATTAATATGGTTCCTCTGCGACCTTTGCGT
   -----+-----+-----+-----+-----+-----+-----+-----+
   E T T S R Q V A S A F I V I L C C A I V
   GGAGACGACCTCCCGCCAGGTGGGCTCGGCTTCATCGTCATCCTCTGTGCGCCATTGT
   -----+-----+-----+-----+-----+-----+-----+-----+
181  CCTCTGCTGGAGGGCGGTCCACCGAGCCGGAAGTAGCAGTAGGAGACAACGCGGTAAAC
   -----+-----+-----+-----+-----+-----+-----+-----+
   V E N L L V L I A V A R N S K F H S A M
   GGTGGAACCTTCTGTGCTCATTTGCGGTGGCCCGAACAGCAAGTTCCTACTCGGCAAT
   -----+-----+-----+-----+-----+-----+-----+-----+
241  CCACCTTTTGAAGACCACGAGTAACGCCACCGGGCTTGTGCTTCAAGGTGAGCCGTTA
   -----+-----+-----+-----+-----+-----+-----+-----+
   Y L F L G N L A A S D L L A G V A F V A
   GTACCTGTTTCTGGGCAACCTGGCCGCTCCGATCTACTGGCAGGCGTGGCCTTCTGTAGC
   -----+-----+-----+-----+-----+-----+-----+-----+
301  CATGGACAAAGACCCGTTGGACCGGCGAGGCTAGATGACCGTCCGCACCGGAAGCATCG
   -----+-----+-----+-----+-----+-----+-----+-----+
   N T L L S G S V T L R L T P V Q W F A R
   CAATACCTTGTCTCTGTGGCTCTGTACGCTGAGGCTGAGCCCTGTGCAGTGGTTTGCCCG
   -----+-----+-----+-----+-----+-----+-----+-----+
361  GTTATGGAACGAGAGACCGAGACAGTGGGACTCCGACTGCGGACACGTACCAAACGGGC
   -----+-----+-----+-----+-----+-----+-----+-----+
   E G S A F I T L S A S V F S L L A I A I
   GGAGGGCTCTGCCTTCATCACGCTCTCGGCTCTGTCTTCAGCCTCTGGCCATCGCCAT
   -----+-----+-----+-----+-----+-----+-----+-----+
421  CCTCCCGAGACGGAAGTAGTGCGAGAGCCGAGACAGAAGTCGGAGGACCGGTAGCGGTA
   -----+-----+-----+-----+-----+-----+-----+-----+
   E R H V A I A K V K L Y Q S D K S C R M
   TGAGCGCCACGTGGCCATTGCCAAGGTCAAGCTGTATGGCAGCGACAAGAGCTGCCGCAT
   -----+-----+-----+-----+-----+-----+-----+-----+
481  ACTCGCGGTGCACCGGTAACGGTTCAGTTCGACATAACCGTCGCTGTTCTCGACGGCGTA
   -----+-----+-----+-----+-----+-----+-----+-----+
   L L L I G A S W L I S L V L G G L P I L
   GCTTCTGCTCATCGGCGCTCTGTGGCTCATCTCGCTGTCTCGGTGGCCTGCCCATCCT
   -----+-----+-----+-----+-----+-----+-----+-----+
541  CGAAGACGAGTAGCCCCGGAGCACCGAGTAGAGCGACAGGAGCCACCGACGGGTAGGA
   -----+-----+-----+-----+-----+-----+-----+-----+
   G W N C L G H L E A C S T V L P L Y A K
   TGGCTGGAACCTGCCTGGGCCACCTCGAGGCTGCTCCACTGTCTGCTCTCTACGCCAA
   -----+-----+-----+-----+-----+-----+-----+-----+
601  ACCGACCTTGACGGACCGGTGGAGCTCCGACGAGCTGACAGGACGGAGAGATGCGGTT
   -----+-----+-----+-----+-----+-----+-----+-----+
   H Y V L C V V T I P S I I L L A I V A L
   GCATTATGTGTGTGCGTGGTGACCATCTTCTCCATCATCCTGTTGGCCATGGTGGCCCT
   -----+-----+-----+-----+-----+-----+-----+-----+
   CGTAATACACGACACGCACCACTGGTAGAAGAGGTAGTAGACACCGGTAGCACCGGGA

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[illegible]

Figure 15B

cDNA sequence of clone pC3-hedg4#36 encoding functional HEDG4 receptor protein.

```

1  ATGGGCAGCTTGTACTCGGAGTACCTGAACCCCAACAAGGTCCAGGAACACTATAATTAT
   -----+-----+-----+-----+-----+-----+
61  TACCCGTCGAACATGAGCCTCATGGACTTGGGGTTGTTCCAGGTCCCTGTGATATTAATA
   -----+-----+-----+-----+-----+-----+
   ACCAAGGAGACGCTGGAAACGCAGGAGACGACCTCCCGCCAGGTGGCCTCGGCCTTCATC
121 -----+-----+-----+-----+-----+-----+
   TGGTTTCCTCTGCGACCTTTGCGTCCTCTGCTGGAGGGCGGTCCACCGGAGCCGGAAGTAG
   -----+-----+-----+-----+-----+-----+
   GTCATCCTCTGTTGCGCCATTGTGGTGGAAAACCTTCTGGTGCTCATTTGCGGTGGCCCCGA
181 -----+-----+-----+-----+-----+-----+
   CAGTAGGAGACAACGCGGTAACACCACCTTTTGGGAAGACCACGAGTAACGCCACCGGGCT
   -----+-----+-----+-----+-----+-----+
   AACAGCAAGTTCACCTCGGCAATGTACCTGTTTCTGGGCAACCTGGCCGCCTCCGATCTA
241 -----+-----+-----+-----+-----+-----+
   TTGTCGTTCAAGGTGAGCCGTTACATGGACAAAGACCCGTTGGACCGGCGGAGGCTAGAT
   -----+-----+-----+-----+-----+-----+
   CTGGCAGGCGTGGCCTTCGTAGCCAATACCTTGCTCTCTGGCTCTGTCACGCTGAGGCTG
301 -----+-----+-----+-----+-----+-----+
   GACCGTCCGCACCGGAAGCATCGGTTATGGAACGAGAGACCGAGACAGTGCAGTCCGAC
   -----+-----+-----+-----+-----+-----+
   ACGCCTGTGCAAGTGGTTTGGCCGGGAGGGCTCTGCCTTCATCACGCTCTCGGCCTCTGTC
361 -----+-----+-----+-----+-----+-----+
   TGCGGACACGTACCAAACGGGGCCCTCCCGAGACGGAAGTAGTGCGAGAGCCGGAGACAG
   -----+-----+-----+-----+-----+-----+
   TTCAGCCTCCTGGCCATCGCCATTGAGCGCCACGTGGCCATTGCCAAGGTCAAGCTGTAT
421 -----+-----+-----+-----+-----+-----+
   AAGTCGAGGACCGGTAGCGGTAACTCGCGGTGCACCGGTAACGGTTCAGTTCGACATA
   -----+-----+-----+-----+-----+-----+
   GGCAGCGACAAGAGCTGCCGATGCTTCTGCTCATCGGGGCCCTCGTGGCTCATCTCGCTG
481 -----+-----+-----+-----+-----+-----+
   CCGTCGCTGTTCTCGACGGCGTACGAAGACGAGTAGCCCCGGAGCACCGAGTAGAGCGAC
   -----+-----+-----+-----+-----+-----+
   GTCCTCGGTGGCCTGCCCATCCTTGGCTGGAACGCTGGGCCACCTCGAGGCCTGCTCC
541 -----+-----+-----+-----+-----+-----+
   CAGGAGCCACCGGACGGGTAGGAACCGACCTTGACGGACCCGGTGGAGCTCCGGACGAGG
   -----+-----+-----+-----+-----+-----+
   ACTGTCTGCTCTCTACGCCAAGCATTATGTGCTGTGCGTGGTGACCATCTTCTCCATC
601 -----+-----+-----+-----+-----+-----+
   TGACAGGACGGAGAGATGCGGTTTCGTAATACACGACACGCACCACTGGTAGAAGAGGTAG
   -----+-----+-----+-----+-----+-----+
   ATCCTGTTGGCCGTCGTGGCCCTGTACGTGCGCATCTACTGCGTGGTCCGCTCAAGCCAC
661 -----+-----+-----+-----+-----+-----+
   TAGGACAACCGGCAGCACCGGGACATGCACGCGTAGATGACGCACCAGGCGAGTTCGGTG
   -----+-----+-----+-----+-----+-----+
   GCTGACATGGCCGCCCCGAGACGCTAGCCCTGCTCAAGACGGTCACCATCGTGCTAGGC
721 -----+-----+-----+-----+-----+-----+
   CGACTGTACCGGGCGGGCGTCTGCGATCGGGACGAGTTCTGCCAGTGGTAGCACGATCCC
   -----+-----+-----+-----+-----+-----+
   GTCTTTATCGTCTGCTGGCTGCCCCGCTTCAGCATCCTCCTTCTGGACTATGCCTGTCCC
780 -----+-----+-----+-----+-----+-----+

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CAGAAATAGCAGACGACCGACGGGCGGAAGTCGTAGGAGGAAGACCTGATACGGACAGGG

781 GTCCACTCCTGCCCCGATCCTCTACAAAGCCCACCTACCTTTTCGCCGTCTCCACCCTGAAT 840
-----+-----+-----+-----+-----+-----+
CAGGTGAGGACGGGCTAGGAGATGTTTCGGGTGATGGAAAAGCGGCAGAGGTGGGACTTA

841 TCCCTGCTCAACCCCGTCATCTACACGTGGCGCAGCCGGGACCTGCGGCGGGAGGTGCTT 900
-----+-----+-----+-----+-----+-----+
AGGGACGAGTTGGGGCAGTAGATGTGCACCGCGTCGGCCCTGGACGCCGCCCTCCACGAA

901 CGGCCGCTGCAGTGCTGGCGGCCGGGGGTGGGGGTGCAAGGACGGAGGCGGGGCGGGACC 960
-----+-----+-----+-----+-----+-----+
GCCGGCGACGTACGACCGCCGGCCCCCACCCTTCCCTGCCTCCGCCCCGCCCTGG

961 CCGGGCCACCACCTCCTGCCACTCCGCAGCTCCAGCTCCCTGGAGAGGGGCATGCACATG 1020
-----+-----+-----+-----+-----+-----+
GGCCCGGTGGTGGAGGACGGTGAGGCGTCGAGGTGAGGGACCTCTCCCCGTACGTGTAC

1021 CCCACGTCACCCACGTTTCTGGAGGGCAACACGGTGGTCTGA 1062
-----+-----+-----+-----+-----+
GGGTGCAGTGGGTGCAAAGACCTCCCGTTGTGCCACCAGACT

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FIGURE 16 A

1 MGSLYSEYLN PNKQSEHTNY TKETLETQET TSQVASAFI VILCCAIIVE
51 NLLVLIIVAR NSKPHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL
101 TPVQWFAREG SAFITLSASV FSLLAIAIER HVAIAKVLY GSDKSCRMIL
151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
201 ILLAIVALYV RIYCVVRSSH ADMAAPOTLA LLKIVTIVLG VFIVCWLPAF
251 SILLLDYACP VHSCPILYKA HYKRAVSTLN SLLNPVIYTW RSRDLRREVL
301 RPLQCWRPGV GVQGRRRGGT PGHLLPLRS SSSLERGMHM PTSPTFLEGN
351 TVV*

Conserved features of G-protein coupled receptors include:

N-terminal extracellular domain:	Residues 1 - 36
TM-I:	Residues 37 - 57
Intracellular loop 1:	Residues 58 - 68
TM-II:	Residues 69 - 92
Extracellular loop 1:	Residues 93 - 111
TM-III:	Residues 112 - 130
Intracellular loop 2:	Residues 131 - 149
TM-IV:	Residues 150 - 168
Extracellular loop 2:	Residues 169 - 185
TM-V:	Residues 186 - 210
Intracellular loop 3:	Residues 211 - 232
TM-VI:	Residues 233 - 254
Extracellular loop 3:	Residues 255 - 266
TM-VII:	Residues 267 - 285
C-terminal cytoplasmic domain:	Residues 286 - 353

Potential post-transcriptional modification sites:

N-glycosylation:	Residues 19
Phosphorylation:	Residues 142, 145, 219, 289, 332, 345
Myristylation:	Residues 141, 318

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Figure 16B

Predicted amino acid sequence of HEDG4 polypeptide encoded by pC3-hedg4#36.

1 MGSLYSEYLN PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE

51 NLLVLIAVAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL

101 TPVQWFAREG SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL

151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTFISI

201 ILLAVVALYV RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAF

251 SILLLDYACP VHSCPILYKA HYLFAVSTLN SLLNPVIYTW RSRDLRREVL

301 RPLQCWRPGV GVQGRRRGGT PGHHLLPLRS SSSLERGMHM PTSPTFLEGN

351 TVV

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Species	Position	Sequence	Length
Human	1	MGSLYSEYLNPKNKVOEHYNYTKETLEQTTSRQVASAFVILCCAIVVE	50
Rat	1	MGGLYSEYLNPKEKVQEHYNYTKETLDMQETPSRKVASAFIILCCAIVVE	50
Human	51	NLLVLIIVARNRSKFHSAMYLFLGNLAASDLAGVAFVANILLSGSVTLRL	100
Rat	51	NLLVLIIVARNRSKFHSAMYLFLGNLAASDLAGVAFVANILLSGPVTLSL	100
Human	101	TPVQWFAREGSAFITLSASVFSLLAIAIERHVALAKVKLYGSDKSCRMLL	150
Rat	101	TPLOWFAREGSAFITLSASVFSLLAIAIERQVAIAKVKLYGSDKSCRMIM	150
Human	151	LIGASWLISLVLGGLPILGWNCIGHLEACSTVPLPYAKHYVLCVVTIFSI	200
Rat	151	LIGASWLISLILGGLPILGWNCIDHLEACSTVPLPYAKHYVLCVVTIFSV	200
Human	201	ILLAIIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLGVPVLCWLPAP	250
Rat	201	ILLAIIVALYVRIYFVVRSSHADVAGPQTLALLKTVTIVLGVPFIICWLPAP	250
Human	251	SILLLDYACPVHSCPILYKAHYKFAVSTLNSLLNPVIYTWRSRDLRREVL	300
Rat	251	SILLLDSTCFVRACFVLYKAHYFFAFATLNSLLNPVIYTWRSRDLRREVL	300
Human	301	RPLQCWRPGVGVGQRRRGGTPGHILLPLRSSSSSLERGLHMPTSPFTLEGN	350
Rat	301	RPLLQWRQGGKATG.RRGGNPGHILLPLRSSSSSLERGLHMPTSPFTLEGN	349
Human	351	TVV* 353	
Rat	350	TVV* 352	

Figure 17B

Alignment of HEDG4 with pC3-hedg4#36 translation product and rat H218 (REDG4). Differences between pC3-hedg4#36 translation product and previously determined HEDG4 polypeptide are indicated in reverse text. Differences between rat and human edg-4 polypeptide sequences are shown in bold, shaded text.

	1					50
HEDG4	MGS	LYSEYLN	PNKVQEHYNY	TKETLETQET	TSRQVASAFI	VILCCAIVVE
HEDG4#36	MGS	LYSEYLN	PNKVQEHYNY	TKETLETQET	TSRQVASAFI	VILCCAIVVE
REDG4	MGS	LYSEYLN	PNKVQEHYNY	TKETLETQET	TSRQVASAFI	VILCCAIVVE
	51					100
HEDG4	NLLVLI	AVAR	NSKFHSAMYL	FLGNLAASDL	LAGVAFVANT	LLSGSVTLRL
HEDG4#36	NLLVLI	AVAR	NSKFHSAMYL	FLGNLAASDL	LAGVAFVANT	LLSGSVTLRL
REDG4	NLLVLI	AVAR	NSKFHSAMYL	FLGNLAASDL	LAGVAFVANT	LLSGSVTLRL
	101					150
HEDG4	TPVQWF	AREG	SAFITLSASV	FSLLAIAIER	HVAIAKVKLY	GSDKSCRMLL
HEDG4#36	TPVQWF	AREG	SAFITLSASV	FSLLAIAIER	HVAIAKVKLY	GSDKSCRMLL
REDG4	TPVQWF	AREG	SAFITLSASV	FSLLAIAIER	HVAIAKVKLY	GSDKSCRMLL
	151					200
HEDG4	LIGASWL	ISL	VLGGLPILGW	NCLGHLEACS	TVLPLYAKHY	VLCVVTIFSI
HEDG4#36	LIGASWL	ISL	VLGGLPILGW	NCLGHLEACS	TVLPLYAKHY	VLCVVTIFSI
REDG4	LIGASWL	ISL	VLGGLPILGW	NCLGHLEACS	TVLPLYAKHY	VLCVVTIFSI
	201					250
HEDG4	ILLAVVAL	YV	RIYCVVRSSH	ADMAAPQTLA	LLKTVTIVLG	VFIVCWLPAF
HEDG4#36	ILLAVVAL	YV	RIYCVVRSSH	ADMAAPQTLA	LLKTVTIVLG	VFIVCWLPAF
REDG4	ILLAVVAL	YV	RIYCVVRSSH	ADMAAPQTLA	LLKTVTIVLG	VFIVCWLPAF
	251					300
HEDG4	SILLLDY	ACP	VHSCPILYKA	HYXFAVSTLN	SLLNPVIYTW	RSRDLRREVL
HEDG4#36	SILLLDY	ACP	VHSCPILYKA	HYXFAVSTLN	SLLNPVIYTW	RSRDLRREVL
REDG4	SILLLDY	ACP	VHSCPILYKA	HYXFAVSTLN	SLLNPVIYTW	RSRDLRREVL
	301					350
HEDG4	RPLQCWR	PGV	GVQRRRRGGT	PGHLLPLRS	SSSLERGMHM	PTSPTFLEGN
HEDG4#36	RPLQCWR	PGV	GVQRRRRGGT	PGHLLPLRS	SSSLERGMHM	PTSPTFLEGN
REDG4	RPLQCWR	PGV	GVQRRRRGGT	PGHLLPLRS	SSSLERGMHM	PTSPTFLEGN
	351					
HEDG4	TVV~					
HEDG4#36	TVV~					
REDG4	TVV~					

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Figure 18A.

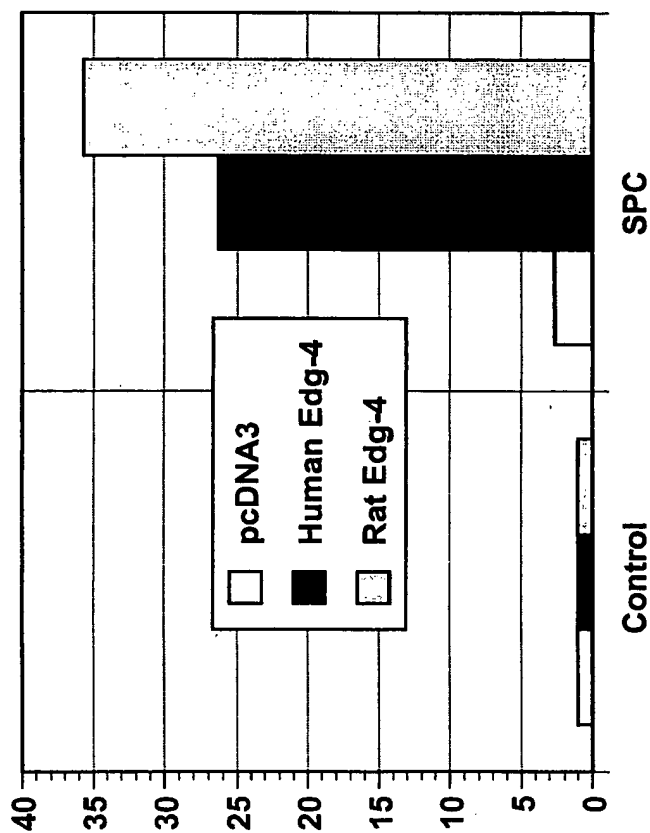


Figure 18B.

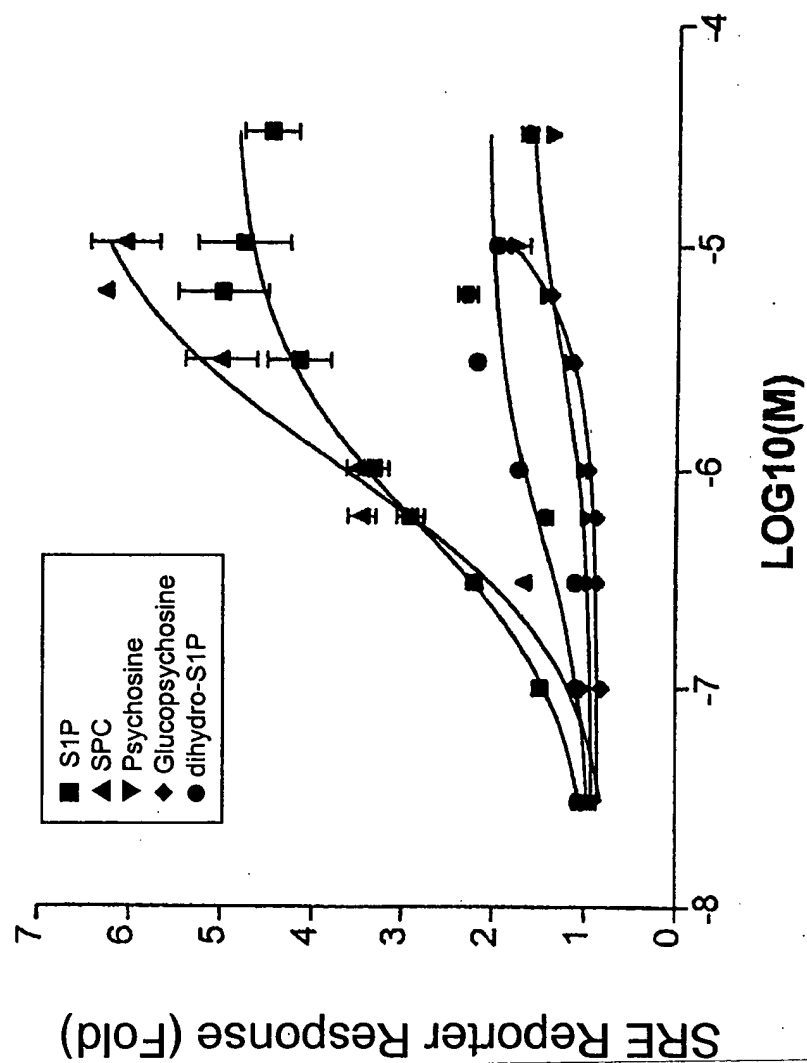


Figure 19.

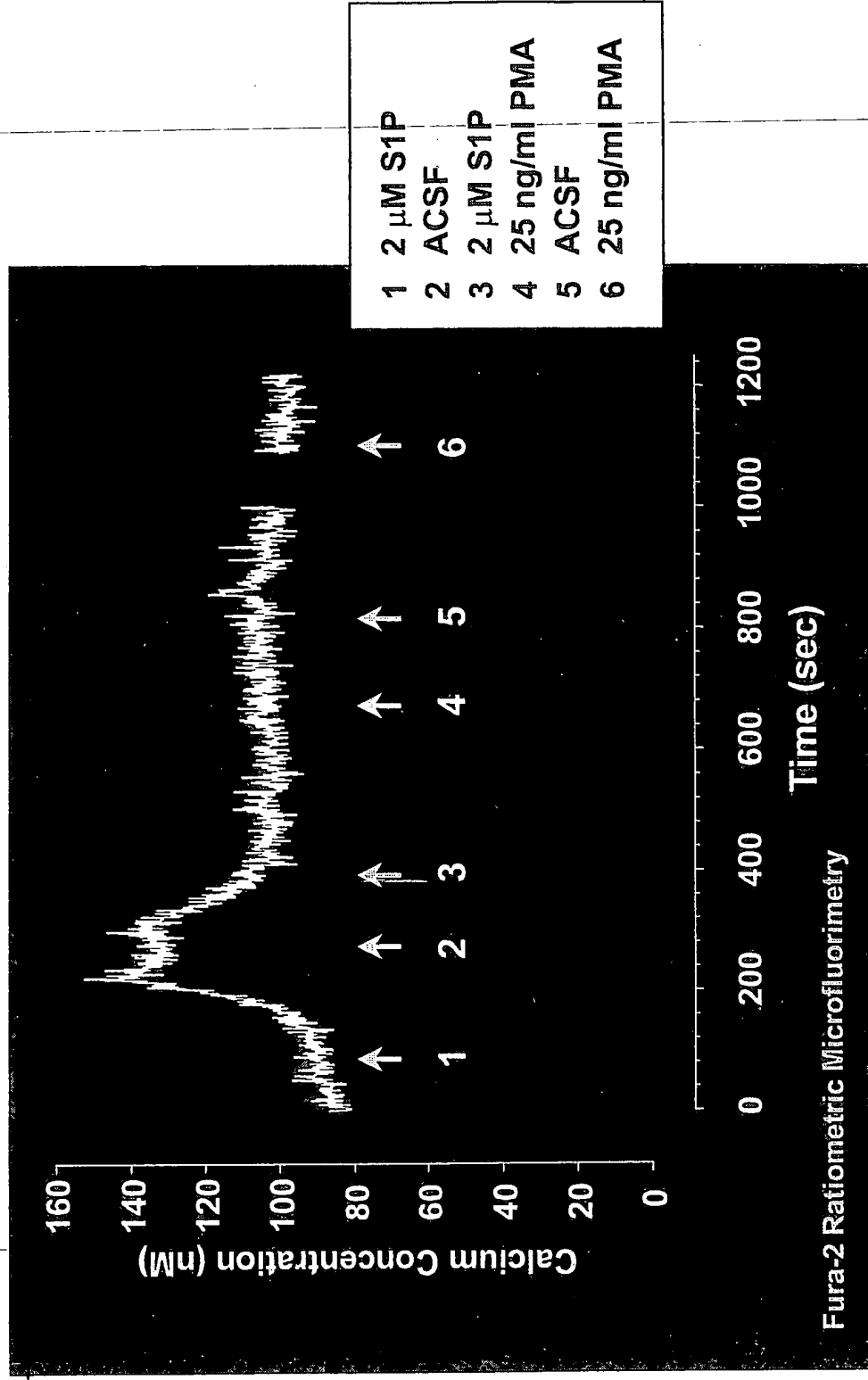


Figure 20.

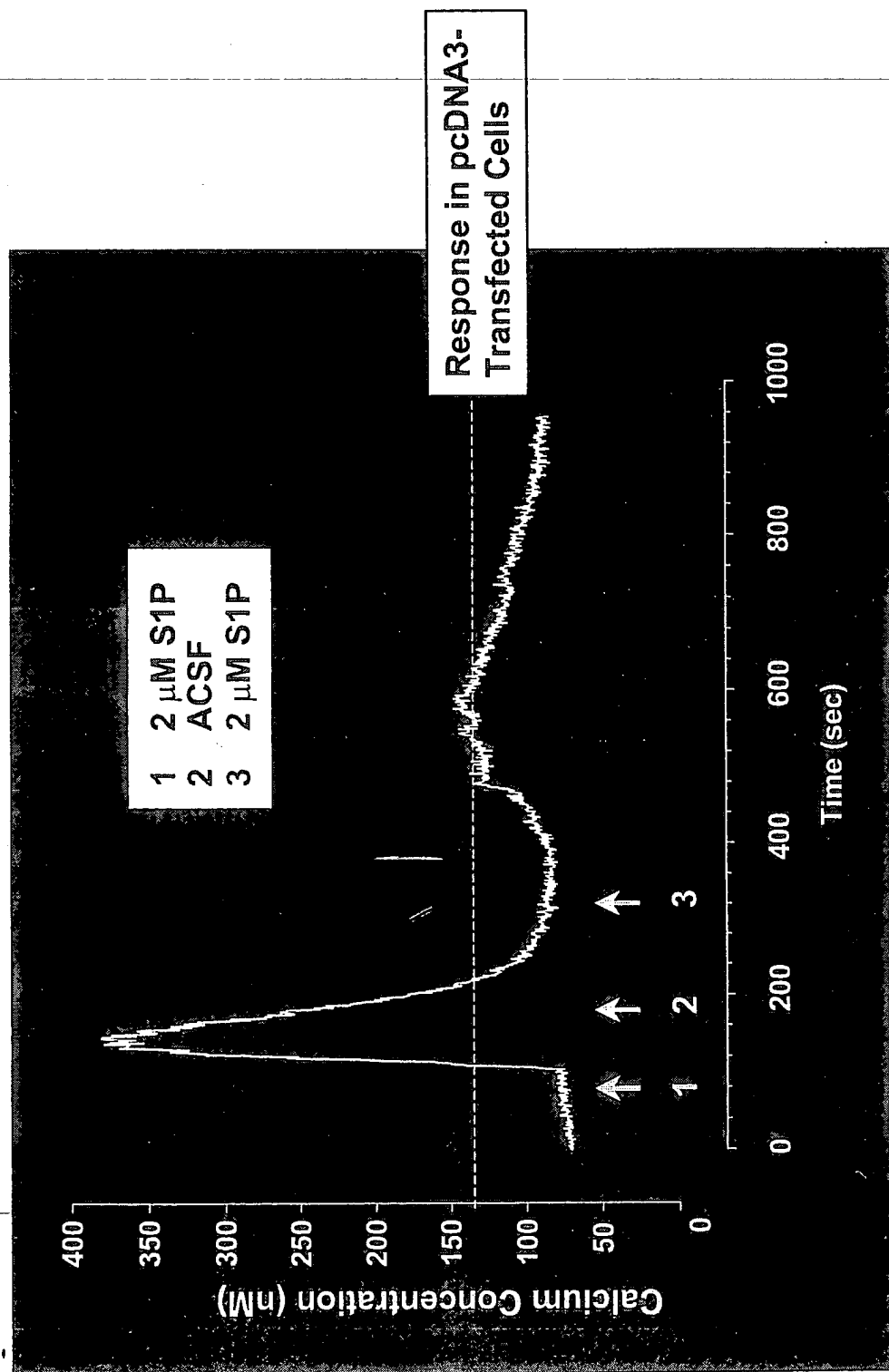


Figure 21. Human Edg-6 Amino Acid Sequence.

1	MVIMGQCYYNETIGFFYNNSGKELSSHWPKDVVVVALGLTVSVLVLLTNLLVIAAIASN	60
61	RRFHQPIIYLLGNLAAADLFAGVAYLFLMFHTGPRTARLSLEGWFLRQGLLDTSLTASVA	120
121	TLLAIAVERHRSVMAVQLHSRLPRGRVVMLIVGVVVAALGLGLLPAHSWHCLCALDRCSR	180
181	MAPLLSRSYLAVWALSSLLVFLLMVAVYTRIFFYVRRRVQMAEHVSCHPRYRETTLSLV	240
241	KTVVILGAFVVCWTPGQVLLLDGLGCESC NVLAVEKYFLLLAEANS LVNAAVYSCRDA	300
301	EMRRTFRLLCCACLRQSTRESVHYTSSAQGGASTRIMLPENGHPLMDSTL*	352

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Figure 22. Human Edg-6 Sequence

1 ATGGTCATCATGGGCCAGTGCTACTACAACGAGACCATCGGCTTCTTCTATAACAACAGT 60
 -----+-----+-----+-----+-----+-----+-----+
 TACCAGTAGTACCCGGTCACGATGATGTTGCTCTGGTAGCCGAAGAAGATATTGTTGTCA
 61 GGCAAAGAGCTCAGCTCCCACTGGCGGCCCAAGGATGTGGTTCGTGGTGGCACTGGGGCTG 120
 -----+-----+-----+-----+-----+-----+-----+
 CCGTTTCTCGAGTCGAGGGTGACCGCCGGGTTCTTACACCAGCACCACCGTGACCCCGAC
 121 ACCGTCAGCGTGCTGGTGCTGCTGACCAATCTGCTGGTCATAGCAGCCATCGCCTCCAAC 180
 -----+-----+-----+-----+-----+-----+-----+
 TGGCAGTCGCACGACCACGACGACTGGTTAGACGACCAGTATCGTCGGTAGCGGAGGTTG
 181 CGCCGCTTCCACCAGCCCATCTACTACCTGCTCGGCAATCTGGCCGCGGCTGACCTCTTC 240
 -----+-----+-----+-----+-----+-----+-----+
 GCGGCGAAGGTGGTTCGGTAGATGATGGACGAGCCGTTAGACCGGCGCCGACTGGAGAAG
 241 GCGGGCGTGGCCTACCTCTTCTCATGTTCCACACTGGTCCCCGCACAGCCCGACTTTCA 300
 -----+-----+-----+-----+-----+-----+-----+
 CGCCCGCACC GGATGGAGAAGGAGTACAAGGTGTGACCAGGGGCGTGTGCGGCTGAAAGT
 301 CTTGAGGGCTGGTTCTTGC GGCAGGGCTTGCTGGACACAAGCCTCACTGCGTCGGTGGCC 360
 -----+-----+-----+-----+-----+-----+-----+
 GAAC'TCCC GACCAAGGACGCCGTCCCGAACGACCTGTGTTTCGGAGTGACGCAGCCACCGG
 361 ACAC'TGCTGGCCATCGCCGTGGAGCGGCACCGCAGTGTGATGGCCGTGCAGCTGCACAGC 420
 -----+-----+-----+-----+-----+-----+-----+
 TGTGACGACCGGTAGCGGCACCTCGCCGTGGCGTCACACTACCGGCACGTGCAGCTGTG
 421 CGCCTGCCCCGTGGCCGCGTGGTTCATGCTCATTTGTGGGCGTGTGGGTGGCTGCCCTGGGC 480
 -----+-----+-----+-----+-----+-----+-----+
 GCGGACGGGGCACCGGCGCACCAGTACGAGTAACACCCGCACACCCACCGACGGGACCCG
 481 CTGGGGCTGCTGCC'TGCCACTCCTGGCACTGCCTCTGTGCCCTGGACCGCTGCTCACGC 540
 -----+-----+-----+-----+-----+-----+-----+
 GACCCCGACGACGGACGGGTGAGGACCGTGACGGAGACACGGGACCTGGCGACGAGTGCG
 541 ATGGCACCCCTGCTCAGCCGCTCCTATTTGGCCGTCTGGGCTCTGTGAGCCCTGCTTGTC 600
 -----+-----+-----+-----+-----+-----+-----+
 TACCGTGGGGACGAGTCGGCGAGGATAAACCGGCAGACCCGAGACAGCTCGGACGAACAG
 601 TTCCTGCTCATGGTGGCTGTGTACACCCGCATTTTCTTCTACGTGCGGCGGCGAGTGCAG 660
 -----+-----+-----+-----+-----+-----+-----+
 AAGGACGAGTACCACCGACACATGTGGGCGTAAAAGAAGATGCACGCCGCCGCTCACGTC
 661 CGCATGGCAGAGCATGTCAGCTGCCACCCCCGCTACCGAGAGACCACGCTCAGCCTGGTC 720
 -----+-----+-----+-----+-----+-----+-----+
 GCGTACCGTCTCGTACAGTCGACGGTGGGGGCGATGGCTCTCTGGTGGAGTCGGACCAG
 721 AAGACTGTTGTATCATCCTGGGGGCGTTTCGTGGTCTGCTGGACACCAGGCCAGGTGGTA 780
 -----+-----+-----+-----+-----+-----+-----+
 TTCTGACAACAGTAGTAGGACCCCCGCAAGCACCAGACGACCTGTGGTCCGGTCCACCAT
 781 CTGCTCCTGGATGGTTTAGGCTGTGAGTCTTGCAATGTCTGGCTGTAGAAAAGTACTTC 840
 -----+-----+-----+-----+-----+-----+-----+
 GACGAGGACCTACCAAATCCGACACTCAGGACGTTACAGGACCGACATCTTTTTCATGAAG

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841 CTACTGcTGGCCGAGGCCAACTCACTGGTCAATGCTGCTGTGTACTCTTGCCGAGATGCT
-----+-----+-----+-----+-----+-----+ 900
GATGACgACCGGCTCCGGTTGAGTGACCAGTTACGACGACACATGAGAACGGCTCTACGA

GAGATGCGCCGCACCTTCCGCCGCCTTCTCTGCTGCGCGTGCC'TCCGCCAGTCCACCCGC
-----+-----+-----+-----+-----+-----+ 960
CTCTACGCGGCGTGGAAGGCGGCGGAAGAGACGACGCGCACGGAGGCGGTGAGGTGGGCG

GAGTCTGTCCACTATACATCCTCTGCCCAGGGAGGTGCCAGCACTCGCATCATGCTTCCC
-----+-----+-----+-----+-----+-----+ 1020
961 CTCAGACAGGTGATATGTAGGAGACGGGTCCCTCCACGGTCGTGAGCGTAGTACGAAGGG

GAGAACGGCCACCCACTGATGGACTCCACCCTTTAG
-----+-----+-----+-----+-----+ 1056
1021 CTCTTGCCGGTGGGTGACTACCTGAGGTGGGAAATC

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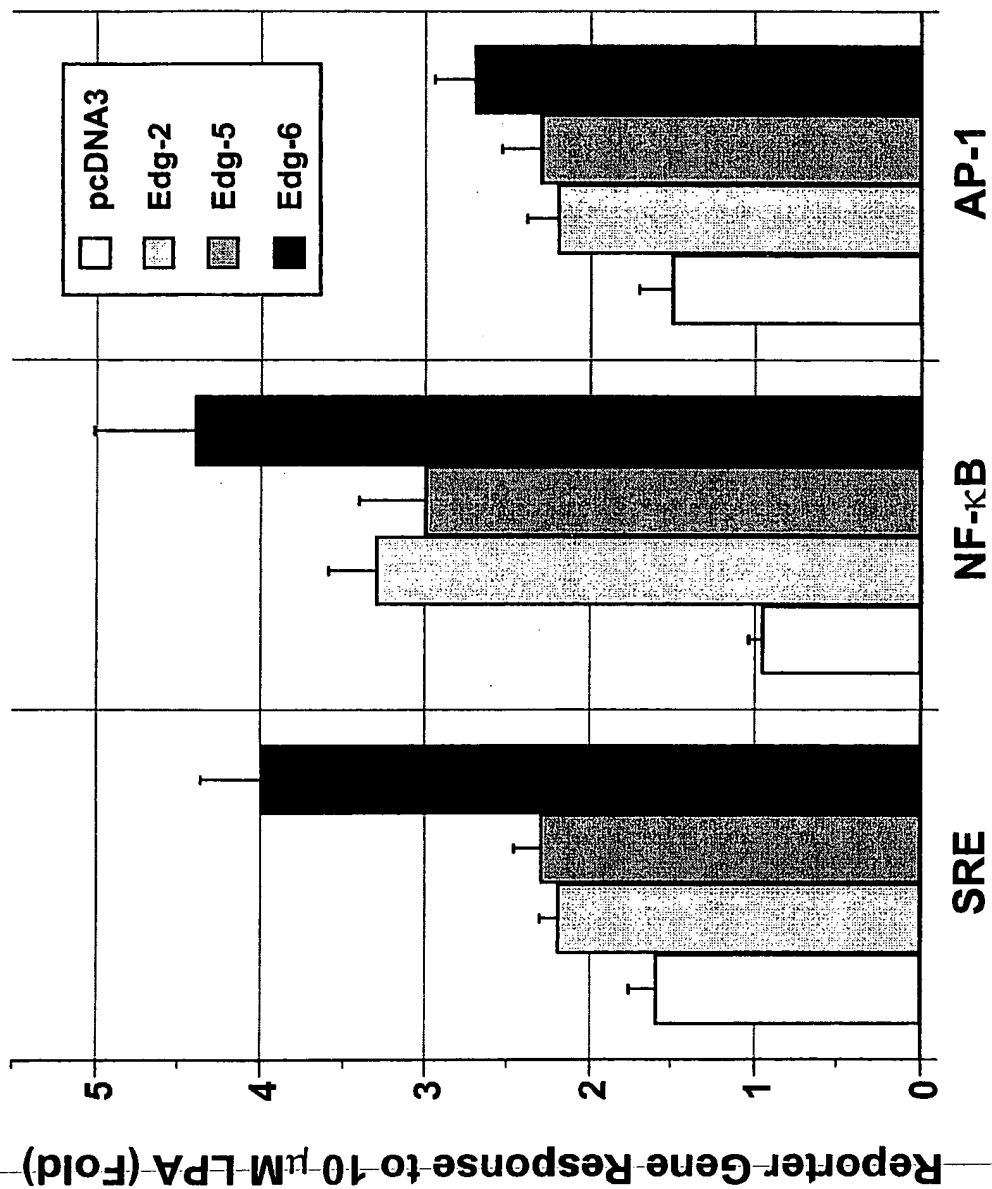


Figure 23.

Figure 24.

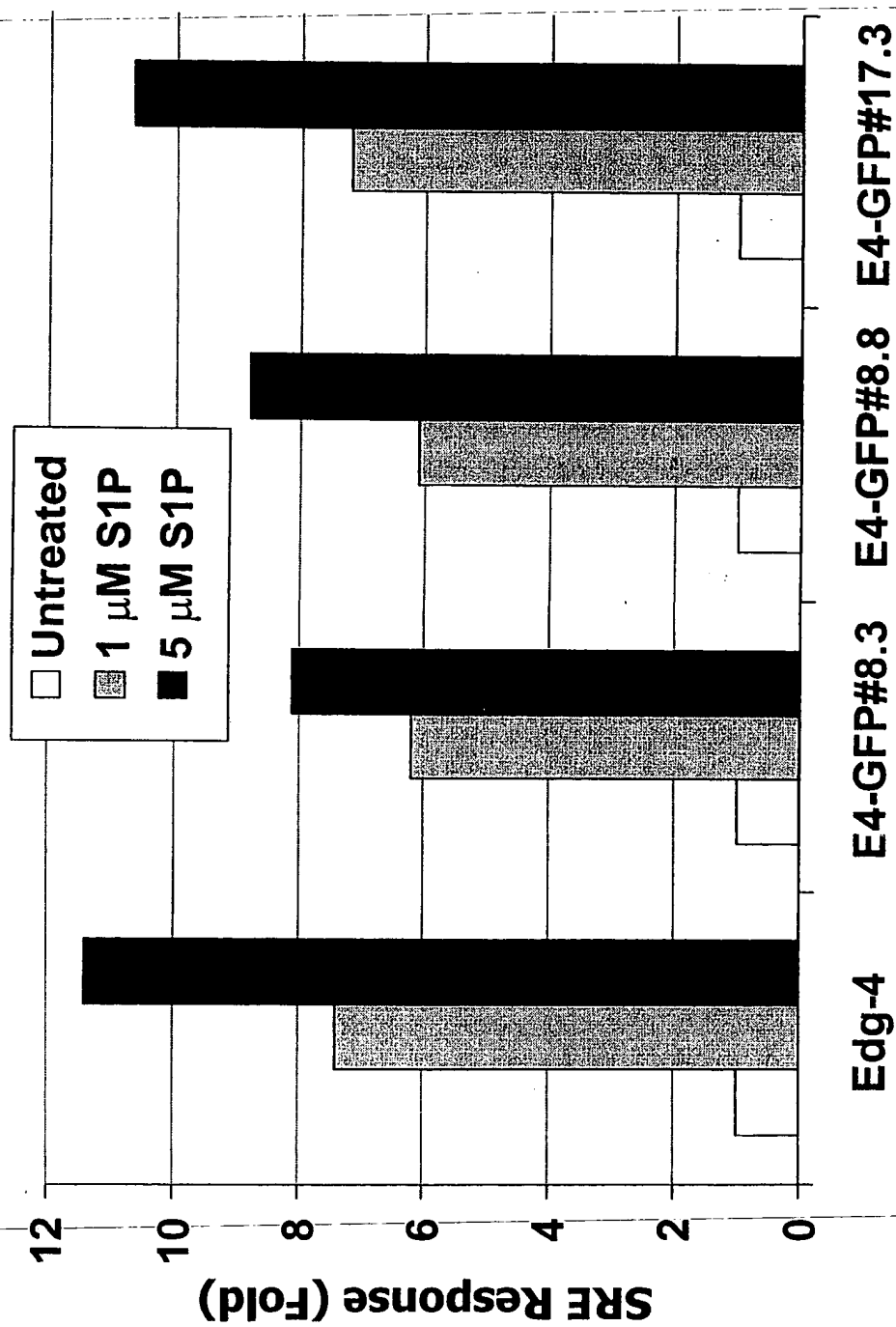


Figure 25.

